SEQUENCE LISTING

<210> Michael Moore
Yen Choo
Aaron Klug

<120> ENGINEERED ZINC FINGER PROTEINS FOR REGULATION OF GENE EXPRESSION

<130> 8325-0038 (S38-US1)

<140> 10/572,886
<141> 2006-10-03

<150> PCT/US2004/030606
<151> 2004-09-17

<150> 60/504,502
<151> 2003-09-19

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<170> PatentIn version 3.3

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Thr Ser Ser Gly Leu Ser Arg
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            20   25   30

Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Asp Asn Arg Asp
            35   40   45

Arg Thr Lys His Thr Lys Ile His Thr Gly Gly Gln Arg Pro Tyr Ala
        50   55   60

Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Asp Arg Lys Thr Leu
65   70   75   80

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Ile Glu His Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg
                85                  90                  95

Ile Cys Met Arg Asn Phe Ser Thr Ser Ser Gly Leu Ser Arg His Ile
            100                 105                 110

Arg Thr His Thr Gly Ser Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
            115                 120                 125

Arg Asn Phe Ser Arg Ser Asp His Leu Ser Glu His Ile Arg Thr His
    130                 135                 140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
145                 150                 155                 160

Thr Ser Ser Asp Arg Thr Lys His Thr Lys Ile His Leu Arg Gln Lys
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Asp Ala Ala Arg Asn
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<212>   DNA
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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc     180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc agatatacg cgttgacatt     240

gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata     300

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atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720

aaaatcaacg ggactttcca aaatgtcgta caactccgc cccattgacg caaatgggcg      780

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc      900

gtttaaactt aagctgatcc actagtccag tgtggtggaa ttcgctagcg ccacc atg      958
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gcc ccc aag aag aag agg aag gtg gga atc gat ggg gta ccc ttc cag     1006
Ala Pro Lys Lys Lys Arg Lys Val Gly Ile Asp Gly Val Pro Phe Gln
            5                   10                  15

tgt cga atc tgc atg cgt aac ttc agt cgt agt gac cac ctg agc cgg     1054
Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Ser Arg
        20                  25                  30

cac atc cgc acc cac aca ggc gag aag cct ttt gcc tgt gac att tgt     1102
His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys
        35                  40                  45

ggg agg aaa ttt gcc gac aac cgg gac cgc aca aag cat acc aag ata     1150
Gly Arg Lys Phe Ala Asp Asn Arg Asp Arg Thr Lys His Thr Lys Ile
50                  55                  60                  65

cac acg ggc gga cag cgg ccg tac gca tgc cct gtc gag tcc tgc gat     1198
His Thr Gly Gly Gln Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp
                    70                  75                  80

cgc cgc ttt tct gac agg aag aca ctt atc gag cat atc cgc atc cac     1246
Arg Arg Phe Ser Asp Arg Lys Thr Leu Ile Glu His Ile Arg Ile His
            85                  90                  95

acc ggt cag aag ccc ttc cag tgt cga atc tgc atg cgt aac ttc agt     1294
Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
            100                 105                 110

acc agc agc ggg ctg agc cgc cac atc cgc acc cac aca gga tct cag     1342
Thr Ser Ser Gly Leu Ser Arg His Ile Arg Thr His Thr Gly Ser Gln
        115                 120                 125

aag ccc ttc cag tgt cga atc tgc atg cgt aac ttc agt cgt agt gac     1390
Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp
130                 135                 140                 145
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10

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cac ctg agc gaa cac att cgc acc cac aca ggc gag aag cct ttt gcc    1438
His Leu Ser Glu His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala
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tgt gac att tgt ggg agg aaa ttt gcc acc agc agc gac cgc aca aag    1486
Cys Asp Ile Cys Gly Arg Lys Phe Ala Thr Ser Ser Asp Arg Thr Lys
            165                 170                 175

cat acc aag ata cac ctg cgc caa aaa gat gcg gcc cgg gga tcc ggc    1534
His Thr Lys Ile His Leu Arg Gln Lys Asp Ala Ala Arg Gly Ser Gly
        180                 185                 190

atg gat gct aag tca cta act gcc tgg tcc cgg aca ctg gtg acc ttc    1582
Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe
    195                 200                 205

aag gat gta ttt gtg gac ttc acc agg gag gag tgg aag ctg ctg gac    1630
Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
210                 215                 220                 225

act gct cag cag atc gtg tac aga aat gtg atg ctg gag aac tat aag    1678
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
                230                 235                 240

aac ctg gtt tcc ttg ggt tat cag ctt act aag cca gat gtg atc ctc    1726
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
            245                 250                 255

cgg ttg gag aag gga gaa gag ccc tgg ctg gtg gag aga gaa att cac    1774
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
        260                 265                 270

caa gag acc cat cct gat tca gag act gca ttt gaa atc aaa tca tca    1822
Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
    275                 280                 285

gtt gac tac aag gac gac gat gac aag taagcttctc gagtctagct          1869
Val Asp Tyr Lys Asp Asp Asp Asp Lys
290                 295

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13

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agtccaatgt ccagcccatg a                                            21
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<210>   37
<211>   25
<212>   DNA
<213>   Artificial Sequence

<220>
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<400>   37
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<210>   38
<211>   21
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<213>   Artificial Sequence

<220>
<223>   Synthetic oligonucleotide sequence for RNA analysis

<400>   38
agagacccat cctgattcag a                                             21


<210>   39
<211>   21
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<213>   Artificial Sequence

<220>
<223>   Synthetic oligonucleotide sequence for RNA analysis

<400>   39
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<210>   40
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<212>   DNA
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<220>
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<400>   40
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<210>   41
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<220>
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<400>  41
ttccgataac gaacgagact ct                                          22


<210>  42
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<220>
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<400>  42
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<210>  43
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<220>
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<400>  43
taactagtta cgcgaccccc gag                                         23


<210>  44
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<220>
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<400>  44
ccttttgcag accacagtcc a                                           21


<210>  45
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<212>  DNA
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<220>
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<400>  45
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<210>  46
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<220>
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<400>   46
cactgccacc cagaagactg tgg                                              23


<210>   47
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<220>
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<400>   47
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<210>   48
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<220>
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<400>   48
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<220>
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<400>   49
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<210>   50
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<210>   51
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<220>
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<400> 51
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<210> 52
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<212> DNA
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<400> 52
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<210> 53
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<220>
<223> Zinc finger protein designed to bind to a target sequence in the rat
     phospholamban gene

<400> 53

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Phe Ser Thr Ser Ala Asp Leu Thr Glu His Ile Arg Ile His Thr Gly
            20   25   30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Ala Ser
        35   40   45

Ala Asn Leu Ser Arg His Ile Arg Thr His Thr Gly Gly Glu Arg Pro
    50   55   60

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Ala Leu
65   70   75   80

Ser Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
                85   90   95

19

Ile Cys Gly Arg Lys Phe Ala Asp Arg Ser Thr Arg Thr Lys His Thr
            100   105   110

Lys Ile His Thr Gly Ser Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
            115   120   125

Arg Asn Phe Ser Arg Ser Asp Val Leu Ser Ala His Ile Arg Thr His
            130   135   140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Lys Lys Phe Ala
145   150   155   160

Asp Arg Ser Asn Arg Ile Lys His Thr Lys Ile His Leu Arg Gln Lys
                165   170   175

Asp Ala Ala Arg
            180